

B.51507

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#10

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**RAW SEQUENCE LISTING**  
**PATENT APPLICATION US/09/488,364**

DATE: 10/30/2000  
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This Raw Listing contains the General Information  
 Section and up to first 5 pages.

ENTERED

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1  <110> APPLICANT: Elledge, Stephen J.
2      Sanchez, Yolanda
3  <120> TITLE OF INVENTION: MAMMALIAN CHECKPOINT GENES AND PROTEINS
4  <130> FILE REFERENCE: 120541-1013
5  <140> CURRENT APPLICATION NUMBER: US/09/488,364
6  <141> CURRENT FILING DATE: 2000-01-12
7  <160> NUMBER OF SEQ ID NOS: 15
8  <170> SOFTWARE: PatentIn Ver. 2.0
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19      35              40              45
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21      50              55              60
22      Glu Asn Val Val Lys Phe Tyr Gly His Arg Arg Glu Gly Asn Ile Gln
23      65              70              75              80
24      Tyr Leu Phe Leu Glu Tyr Cys Ser Gly Gly Glu Leu Phe Asp Arg Ile
25      85              90              95
26      Glu Pro Asp Ile Gly Met Pro Glu Pro Asp Ala Gln Arg Phe Phe His
27      100             105             110
28      Gln Leu Met Ala Gly Val Val Tyr Leu His Gly Ile Gly Ile Thr His
29      115             120             125
30      Arg Asp Ile Lys Pro Glu Asn Leu Leu Leu Asp Glu Arg Asp Asn Leu
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32      Lys Ile Ser Asp Phe Gly Leu Ala Thr Val Phe Arg Tyr Asn Asn Arg
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36      Glu Leu Leu Lys Arg Arg Glu Phe His Ala Glu Pro Val Asp Val Trp
37      180             185             190
38      Ser Cys Gly Ile Val Leu Thr Ala Met Leu Ala Gly Glu Leu Pro Trp
39      195             200             205
40      Asp Gln Pro Ser Asp Ser Cys Gln Glu Tyr Ser Asp Trp Lys Glu Lys
41      210             215             220
42      Lys Thr Tyr Leu Asn Pro Trp Lys Lys Ile Asp Ser Ala Pro Leu Ala
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44      Leu Leu His Lys Ile Leu Val Glu Asn Pro Ser Ala Arg Ile Thr Ile
  
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49          275          280          285
50    Gly Phe Ser Lys His Ile Gln Ser Asn Leu Asp Phe Ser Pro Val Asn
51          290          295          300
52    Ser Ala Ser Ser Glu Glu Asn Val Lys Tyr Ser Ser Ser Gln Pro Glu
53    305          310          315          320
54    Pro Arg Thr Gly Leu Ser Leu Trp Asp Thr Ser Pro Ser Tyr Ile Asp
55          325          330          335
56    Lys Leu Val Gln Gly Ile Ser Phe Ser Gln Pro Thr Cys Pro Asp His
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59          355          360          365
60    Pro Trp Gln Arg Leu Val Lys Arg Met Thr Arg Phe Phe Thr Lys Leu
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63    385          390          395          400
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65          405          410          415
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82          20          25          30
83    Gln Ala Val Ala Val Lys Ile Val Asp Met Lys Arg Ala Ile Asp Cys
84          35          40          45
85    Pro Gln Asn Ile Lys Lys Glu Ile Cys Ile Asn Lys Met Leu Ser His
86          50          55          60
87    Glu Asn Val Val Lys Phe Tyr Gly His Arg Arg Glu Gly His Ile Gln
88          65          70          75          80
89    Tyr Leu Phe Leu Glu Tyr Cys Ser Gly Gly Glu Leu Phe Asp Arg Ile
90          85          90          95
91    Glu Pro Asp Ile Gly Met Pro Glu Gln Asp Ala Gln Arg Phe Phe His
92          100          105          110
93    Gln Leu Met Ala Gly Val Val Tyr Leu His Gly Ile Gly Ile Thr His
94          115          120          125

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**RAW SEQUENCE LISTING**  
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100     165                      170                      175
101     Glu Leu Leu Lys Arg Lys Glu Phe His Ala Glu Pro Val Asp Val Trp
102     180                      185                      190
103     Ser Cys Gly Ile Val Leu Thr Ala Met Leu Ala Gly Glu Leu Pro Trp
104     195                      200                      205
105     Asp Gln Pro Ser Asp Ser Cys Gln Glu Tyr Ser Asp Trp Lys Glu Lys
106     210                      215                      220
107     Lys Thr Tyr Leu Asn Pro Trp Lys Lys Ile Asp Ser Ala Pro Leu Ala
108     225                      230                      235                      240
109     Leu Leu His Lys Ile Leu Val Glu Thr Pro Ser Ala Arg Ile Thr Ile
110     245                      250                      255
111     Pro Asp Ile Lys Lys Asp Arg Trp Tyr Asn Lys Pro Leu Asn Arg Gly
112     260                      265                      270
113     Ala Lys Arg Pro Arg Ala Thr Ser Gly Gly Met Ser Glu Ser Ser Ser
114     275                      280                      285
115     Gly Phe Ser Lys His Ile His Ser Asn Leu Asp Phe Ser Pro Val Asn
116     290                      295                      300
117     Asn Gly Ser Ser Glu Glu Thr Val Lys Phe Ser Ser Ser Gln Pro Glu
118     305                      310                      315                      320
119     Pro Arg Thr Gly Leu Ser Leu Trp Asp Thr Gly Pro Ser Asn Val Asp
120     325                      330                      335
121     Lys Leu Val Gln Gly Ile Ser Phe Ser Gln Pro Thr Cys Pro Glu His
122     340                      345                      350
123     Met Leu Val Asn Ser Gln Leu Leu Gly Thr Pro Gly Phe Ser Gln Asn
124     355                      360                      365
125     Pro Trp Gln Arg Leu Val Lys Arg Met Thr Arg Phe Phe Thr Lys Leu
126     370                      375                      380
127     Asp Ala Asp Lys Ser Tyr Gln Cys Leu Lys Glu Thr Phe Glu Lys Leu
128     385                      390                      395                      400
129     Gly Tyr Gln Trp Lys Lys Ser Cys Met Asn Gln Val Thr Val Ser Thr
130     405                      410                      415
131     Thr Asp Arg Arg Asn Asn Lys Leu Ile Phe Lys Ile Asn Leu Val Glu
132     420                      425                      430
133     Met Asp Glu Lys Ile Leu Val Asp Phe Arg Leu Ser Lys Gly Asp Gly
134     435                      440                      445
135     Leu Glu Phe Lys Arg His Phe Leu Lys Ile Lys Gly Lys Leu Ser Asp
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137     Val Val Ser Ser Gln Lys Val Trp Phe Pro Val Thr
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139 &lt;210&gt; SEQ ID NO 3

140 &lt;211&gt; LENGTH: 1761

141 &lt;212&gt; TYPE: DNA

142 &lt;213&gt; ORGANISM: Homo sapiens

143 &lt;400&gt; SEQUENCE: 3

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**RAW SEQUENCE LISTING**  
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147      agaaaatatt aagaaagaga tctgtatcaa taaaatgcta aatcatgaaa atgtagtaaa 240
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150      attcttccat caactcatgg caggggtggt ttatctgcat ggtattggaa taactcacag 420
151      ggatattaaa ccagaaaatc ttctgttgga tgaaagggat aacctcaaaa tctcagactt 480
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155      ccaacccagt gacagctgtc aggagtattc tgactggaaa gaaaaaaaaa catacctcaa 720
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181      agctgttgca gtgaaaattg tagacatgaa gcggggccata gactgtccac aaaatattaa 180
182      gaaagagatc tgcatacaata aaatgttaag ccacgagaat gtagtgaaat tctatggcca 240
183      caggagggaa ggccatatcc agtatctggt tctggagtag ttagtgaggag gagaactttt 300
184      tgatagaatt gagccagaca tagggatgcc tgaacaagat gctcagagggt tcttccacca 360
185      actcatggca ggggtggttt atcttcatgg aatttgaata actcacaggg atattaaacc 420
186      agaaaacctc ctcttggatg aaagggataa cctcaaaaatc tctgactttg gcttggcaac 480
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188      tgttgctccg gagcttctaa agagaaaaga atttcatgca gaaccagttg atgtttggtc 600
189      ctgtggaata gtacttactg caatgttggc tggagaattg ccgtgggacc agcccagtga 660
190      tagctgtcag gaatattctg atttgaaaga aaaaaaaacc tatctcaatc cttggaaaaa 720
191      aattgattct gctcctctgg ctttgcctta taaaattcta gttgagactc catcagcaag 780
192      gatcaccatc ccagacatta agaaagatag atggtacaac aaaccactta acagaggagc 840
193      aaagaggcca cgcgccacat caggtggtat gtcagagtct tctagtggat tctctaagca 900
194      cattcattcc aatttggact tttctccagt aaataatggt tccagtgaag aaaccgtgaa 960

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197      gcttgtaaac agtcagttac tcggtacccc tggattttca cagaaccctt ggcagcgctt 1140
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200      tgtatcaaca actgatagaa gaaacaataa gttgattttc aaaataaatt tggtagaaat 1320
201      ggatgagaag atactggttg acttccgact ttctaagggt gatggattag agttcaagag 1380
202      acacttcctg aagattaaag ggaagctcag cgatgttggt agcagccaga aggtttgggt 1440
203      tcctgttaca tgaggaagct gtcagctctg cacattcctg gtgaatagag tgctgctatg 1500
204      tgacatTTTT cttcctagag aagattatct attctgcaaa ctgcaaacaa tagttgttga 1560
205      agagttctct tcccattacc caaacatctt ccgatttgta gtgtttggca taaaataact 1620
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208      cagcttttat acccatgtag tagtatcact tttgaaaaat caaaagcttg tttcatccca 1800
209      agcaaaatat tttcttctct gcctatttaa ttgtaaggat gaataaacac agaccatata 1860
210      cagttgattg gttcatgaat gaggccagcc acaaaaatgt gtatgttaat gtatgtactg 1920
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221      <223> OTHER INFORMATION: The nucleic acid in this position can be either
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223      <220> FEATURE:
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236      <211> LENGTH: 17
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238      <213> ORGANISM: Artificial Sequence
239      <220> FEATURE:
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